(FILE 'HOME' ENTERED AT 14:51:15 ON 01 MAY 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 14:51:18 ON 01 MAY 2003

L1 14005 S GLUCOSE (1N) DEHYDROGENASE
L2 112142 S FUSION (1N) PROTEIN
L3 40 S L1 AND L2
L4 28 DUP REM L3 (12 DUPLICATES REMOVED)
L5 4 S L4 AND TAG

FILE 'STNGUIDE' ENTERED AT 15:12:27 ON 01 MAY 2003

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 15:13:26 ON 01 MAY 2003

L6 7 S L1 AND (FUSION OR CHIMER?) AND TAG
L7 5 DUP REM L6 (2 DUPLICATES REMOVED)
L8 42 S L1 AND (FUSION OR CHIMER?) AND (TAG OR GFP OR GALACTOSIDASE)
L9 22 DUP REM L8 (20 DUPLICATES REMOVED)

	Type	Hits	Search Text	DBs
1	BRS	109	fusion and (glucose near2 dehydrogenase) and tag	USPAT; US-PGPUB; EPO; JPO; DERWENT;
2	BRS	310	fusion and (glucose near2 dehydrogenase)	USPAT; US-PGPUB; EPO; JPO; DERWENT;
3	BRS	1236	glucose near1 dehydrogenase	USPAT; US-PGPUB; EPO; JPO; DERWENT;
4	BRS	142	(glucose near1 dehydrogenase) and (fusion near1 protein)	USPAT; US-PGPUB; EPO; JPO; DERWENT;
5	BRS	289	"4751180"	USPAT; US-PGPUB; EPO; JPO; DERWENT;
6	IS&R	2	("4751180").PN.	USPAT; US-PGPUB; EPO; JPO; DERWENT;
7	BRS	0	(("4751180").PN.) and tag	USPAT; US-PGPUB; EPO; JPO; DERWENT;
8	BRS	1	(("4751180").PN.) and detect	USPAT; US-PGPUB; EPO; JPO; DERWENT;
9	BRS	2	(("4751180").PN.) andgalactosidase	USPAT; US-PGPUB; EPO; JPO; DERWENT;
10	BRS	1	(("4751180").PN.) and galactosidase	USPAT; US-PGPUB; EPO; JPO; DERWENT;
11	BRS	1236	glucose near1 dehydrogenase	USPAT; US-PGPUB; EPO; JPO; DERWENT;
12	BRS	198	(glucose near1 dehydrogenase) and fusion and (tag or galactosidase)	USPAT; US-PGPUB; EPO; JPO; DERWENT;
13	BRS	28	(glucose near1 dehydrogenase) and fusion and (tag or galactosidase) and gfp	USPAT; US-PGPUB; EPO; JPO; DERWENT;
14	BRS	102	(glucose near1 dehydrogenase) and (chimeric or fusion) and tag	USPAT; US-PGPUB; EPO; JPO; DERWENT;

ANSWER 17 OF 22 MEDLINE DUPLICATE 8

AN 92000598 MEDLINE
DN 92000598 PubMed ID: 1367576
TI Inducible high-level expression of heterologous genes in Bacillus megaterium using the regulatory elements of the xylose-utilization operon.
AU Rygus T; Hillen W
CS Lehrstuhl fur Mikrobiologie, Institut fur Mikrobiologie und Biochemieder Friedrich-Alexander Universitat Erlangen-Nurnberg, Federal Republic of Germany.
SO APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, (1991 Aug) 35 (5) 594-9. Journal code: 8406612. ISSN: 0175-7598.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Biotechnology
EM 199110
ED Entered STN: 19950809
Last Updated on STN: 20000303
Entered Medline: 19911030
AB We have constructed a shuttle plasmid for Bacillus megaterium and Escherichia coli that contains the promoter and repressor gene of the B. megaterium-borne operon for xylose utilization. A polylinker downstream of the promoter allows versatile cloning of genes under its transcriptional control. We have placed gdhA (encoding **glucose dehydrogenase**) from B. megaterium, lacZ (encoding beta-**galactosidase**) from E. coli, mro (encoding mutarotase) from Acinetobacter calcoaceticus, and human puk (encoding single-chain urokinase-like plasminogen activator, rscuPA) under xylose control in this vector. All four genes were between 130-fold and 350-fold inducible by 0.5% xylose in the growth medium in B. megaterium. Enzymatically active **glucose dehydrogenase** and mutarotase accumulated to 20% and 30% of the total soluble protein, respectively. beta-**Galactosidase** and rscuPA were also expressed at a high level. A gel analysis of the products demonstrated their proteolytic stability in the cytoplasm, even up to 5 h after induction. The expression properties of this new host-vector system are discussed in comparison to the ones available for B. subtilis and E. coli.

ANSWER 24 OF 28 MEDLINE DUPLICATE 5

AN 93286127 MEDLINE

DN 93286127 PubMed ID: 8509415

TI Topological analysis of quinoprotein **glucose dehydrogenase** in Escherichia coli and its ubiquinone-binding site.

AU Yamada M; Sumi K; Matsushita K; Adachi O; Yamada Y

CS Department of Biological Chemistry, Faculty of Agriculture, Yamaguchi University, Japan.

SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1993 Jun 15) 268 (17) 12812-7.
Journal code: 2985121R. ISSN: 0021-9258.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199307

ED Entered STN: 19930723
Last Updated on STN: 19970203
Entered Medline: 19930713

AB Topological structure of quinoprotein **glucose dehydrogenase** in the inner membrane of Escherichia coli was determined by constructing **protein fusions** with alkaline phosphatase or beta-galactosidase. Analysis of the fusions revealed that the dehydrogenase possesses five membrane-spanning segments, and the N-terminal and C-terminal portions resided at the cytoplasmic and periplasmic side of the membrane, respectively. These results agreed with the hydropathy profile based on its primary structure. The topological structure suggests that the predicted binding site of the prosthetic group pyrroloquinoline quinone is located at the periplasmic side and that the amino acid residues corresponding to those that were presumed to interact with ubiquinone in one subunit of mitochondrial NADH dehydrogenase also occur at the periplasmic side. When the purified **glucose dehydrogenase** and cytochrome o ubiquinol oxidase were reconstituted together with ubiquinone into liposomes, a membrane potential could be generated by the electron transfer at the site of the ubiquinol oxidase but not of the dehydrogenase. These results suggest that **glucose dehydrogenase** has a ubiquinone reacting site close to the periplasmic side of the membrane, and thus its electron transfer to ubiquinone appears to be incapable of forming a proton electrochemical gradient across the inner membrane of E. coli.